

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: SmithKline Beecham, Corporation
- (ii) TITLE OF INVENTION: Recombinant Feline Coronavirus S Proteins
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SmithKline Beecham Corporation
  - (B) STREET: 709 Swedeland Road
  - (C) CITY: King of Prussia
  - (D) STATE: PA
  - (E) COUNTRY: USA
  - (F) ZIP: 19406-2799
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/698,927
  - (B) FILING DATE: 13-MAY-1991
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/613,066
  - (B) FILING DATE: 14-NOV-1990
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: King, William T.
  - (B) REGISTRATION NUMBER: 30,954
  - (C) REFERENCE/DOCKET NUMBER: SBC 14532B
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (215) 270-5015
  - (B) TELEFAX: (215) 270-5090

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCCCCCGG GTATGATTGT GCTCGTAACT TGCCTCTTG

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAATACCCGG GCACTGGTAA TGCACGTGGT AAACC

35

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTATCCCGG GCACGCTCAA GCACTGCTAC CTGGG

35

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGATCCCGG GGTACAATCT GGTATGGGTG CTACAG

36

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTTACCCGG GGTGGTTATG GTCAACCCAT AGCCTCGAC

39

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGTGACCCGG GCGCCATGTG ATGTAAGCGC ACAAGCGGC

39

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAATCCCGG GGGGTGCCAG ACTTGAAAC ATGGAGG

37

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTACCCGG GGGTGCACTT GGTGGTGGCG CCGTGGC

37

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGGTCCCGG GCTCAGTCTC AGAGATTCGG ATTCTGTGG

39

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAATAGGCC TGGTTTACCA CGTGCATTAC CAGTGC

36

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATTAGGCC TCCCAGGTAG CAGTGCTTGA GCGTG

35

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAATAAGGCC TCTGTAGCAC CCATACCAGA TTGTAC

36

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTAGTAGGCC TGTGAGGCT ATGGGTTGAC CATAACCAC

39

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAACAAGGCC TGCCGCTTGT GCGCTTACAT CACATGGCG

39

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCAAAGGCC TCCTCCATGT TTTCAAGTCT GGCACCC

37

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTATAAGGCC TGCCACGGCG CCACCACCAA GTGCACC

37

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATTAAGGCC TCCACAGAAT CCGAATCTCT GAGACTGAG

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TAAATAGGCC TTTAGTGGAC ATGCACTTTT TCAATTGG

38

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT CCC GAA TTC CAA GAA AAA ACA CAA TCT CTG TTT GCC AAC GCA	48
Met Asp Pro Glu Phe Gln Glu Lys Thr Gln Ser Leu Phe Ala Asn Ala	
1 5 10 15	
TTT GGC TAC CCT GCC ACT CAC ACC ATT CAG GGC CCT GGC CGC GTG AAT	96
Phe Gly Tyr Pro Ala Thr His Thr Ile Gln Gly Pro Gly Arg Val Asn	
20 25 30	
TTG ATT GGT GAA CAC ACC GAC TAC AAC GAC GGT TTC GTT CTG CCC TGC	144
Leu Ile Gly Glu His Thr Asp Tyr Asn Asp Gly Phe Val Leu Pro Cys	
35 40 45	
GCG ATT GAT TAT CAA ACC GTG ATC CCT AAT ACC CGG GGC ACT GGT AAT	192
Ala Ile Asp Tyr Gln Thr Val Ile Pro Asn Thr Arg Gly Thr Gly Asn	
50 55 60	
GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT	240
Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser	
65 70 75 80	
GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC	288
Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro	
85 90 95	
CTT TTA AAA CAT GGG TTA GTG TGT ATA ACT AAA AAT CGC CAT ATT AAC	336
Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn	
100 105 110	
TAT GAA CAA TTC GCC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT	384
Tyr Glu Gln Phe Ala Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala	
115 120 125	
GAC AGA AAA ATT CCC TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA	432
Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys	
130 135 140	
ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT	480
Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser	
145 150 155 160	
GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC	528
Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val	
165 170 175	
ACA CTT TTG TAT TCA CGC AGC AGC ACT GCT ACC TGG GAG GCC	570
Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu Ala	
180 185 190	
TAG	573

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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Met Asp Pro Glu Phe Gln Glu Lys Thr Gln Ser Leu Phe Ala Asn Ala
 1          5          10          15
Phe Gly Tyr Pro Ala Thr His Thr Ile Gln Gly Pro Gly Arg Val Asn
          20          25          30
Leu Ile Gly Glu His Thr Asp Tyr Asn Asp Gly Phe Val Leu Pro Cys
          35          40          45
Ala Ile Asp Tyr Gln Thr Val Ile Pro Asn Thr Arg Gly Thr Gly Asn
          50          55          60
Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser
          65          70          75          80
Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro
          85          90          95
Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn
          100          105          110
Tyr Glu Gln Phe Ala Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala
          115          120          125
Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys
          130          135          140
Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser
          145          150          155          160
Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val
          165          170          175
Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu Ala
          180          185          190

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## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..4362

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG	ATT	GTG	CTC	GTA	ACT	TGC	CTC	TTG	TTG	TTA	TGT	TCA	TAC	CAC	ACA	48
Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr	
1				5				10						15		
GTT	TTG	AGT	ACA	ACA	AAT	AAT	GAA	TGC	ATA	CAA	GTT	AAC	GTA	ACA	CAA	96
Val	Leu	Ser	Thr	Thr	Asn	Asn	Glu	Cys	Ile	Gln	Val	Asn	Val	Thr	Gln	
			20				25						30			
TTG	GCT	GGC	AAT	GAA	AAC	CTT	ATC	AGA	GAT	TTT	CTG	TTT	AGT	AAC	TTT	144
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Ser	Asn	Phe	
		35					40					45				
AAA	GAA	GAA	GGA	AGT	GTA	GTT	GTT	GGT	GGT	TAT	TAC	CCT	ACA	GAG	GTG	192
Lys	Glu	Glu	Gly	Ser	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val	
	50					55					60					
TGG	TAC	AAC	TGC	TCT	AGA	ACA	GCA	CAA	ACT	ACT	GCC	TTT	CAG	TAT	TTT	240
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Gln	Thr	Thr	Ala	Phe	Gln	Tyr	Phe	
65					70				75						80	
AAT	AAT	ATA	CAT	GCC	TTT	TAT	TTT	GTT	ATG	GAA	GCC	ATG	GAA	AAT	AGC	288
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Val	Met	Glu	Ala	Met	Glu	Asn	Ser	
				85					90					95		
ACT	GGT	AAT	GCA	CGT	GGT	AAA	CCA	TTA	TTA	TTT	CAT	GTG	CAT	GGT	GAG	336
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu	
			100					105					110			
CCT	GTT	AGT	GTT	ATT	ATA	TAT	ATA	TCG	GCT	TAT	AGG	GAT	GAT	GTG	CAA	384
Pro	Val	Ser	Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln	
		115					120					125				
CAA	AGG	CCC	CTT	TTA	AAA	CAT	GGG	TTA	GTG	TGC	ATA	ACT	AAA	AAT	CGC	432
Gln	Arg	Pro	Leu	Leu	Lys	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	
	130					135					140					
CAT	ATT	AAC	TAT	GAA	CAA	TTC	ACC	TCC	AAC	CAG	TGG	AAT	TCC	ACA	TGT	480
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	
145					150					155					160	
ACG	GGT	GCT	GAC	AGA	AAA	ATT	CCT	TTC	TCT	GTC	ATA	CCC	ACG	GAC	AAT	528
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	
				165					170					175		
GGA	ACA	AAA	ATC	TAT	GGT	CTT	GAG	TGG	AAT	GAT	GAC	TTT	GTT	ACA	GCT	576
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	
			180					185					190			
TAT	ATT	AGT	GGT	CGT	TCT	TAT	CAC	TTG	AAC	ATC	AAT	ACT	AAT	TGG	TTT	624
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	
		195					200					205				
AAC	AAT	GTC	ACA	CTT	TTG	TAT	TCA	CGC	TCA	AGC	ACT	GCT	ACC	TGG	GAA	672
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
TAC	AGT	GCT	GCA	TAT	GCT	TAC	CAA	GGT	GTT	TCT	AAC	TTC	ACT	TAT	TAC	720
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235					240	
AAG	TTA	AAT	AAC	ACC	AAT	GGT	CTA	AAA	ACC	TAT	GAA	TTA	TGT	GAA	GAT	768
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	
				245					250					255		



TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270	816
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GCT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Ala Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

AGC	TTT	TTC	ACA	CAC	ACC	GCT	GTC	AAT	ATA	ACC	ATT	GAT	CTT	GGT	ATG	1632
Ser	Phe	Phe	Thr	His	Thr	Ala	Val	Asn	Ile	Thr	Ile	Asp	Leu	Gly	Met	
530						535					540					
AAG	CTT	AGT	GGT	TAT	GGT	CAA	CCC	ATA	GCC	TCG	ACA	CTA	AGT	AAC	ATC	1680
Lys	Leu	Ser	Gly	Tyr	Gly	Gln	Pro	Ile	Ala	Ser	Thr	Leu	Ser	Asn	Ile	
545					550					555					560	
ACA	CTA	CCA	ATG	CAG	GAT	AAC	AAT	ACT	GAT	GTG	TAC	TGT	ATT	CGT	TCT	1728
Thr	Leu	Pro	Met	Gln	Asp	Asn	Asn	Thr	Asp	Val	Tyr	Cys	Ile	Arg	Ser	
				565					570					575		
AAC	CAA	TTC	TCA	GTT	TAT	GTT	CCT	TCC	ACT	TGC	AAA	AGT	TCT	TTA	TGG	1776
Asn	Gln	Phe	Ser	Val	Tyr	Val	Pro	Ser	Thr	Cys	Lys	Ser	Ser	Leu	Trp	
			580					585					590			
GAC	AAT	ATT	TTT	AAT	CAA	GAC	TGC	ACG	GAT	GTT	TTA	GAG	GCT	ACA	GCT	1824
Asp	Asn	Ile	Phe	Asn	Gln	Asp	Cys	Thr	Asp	Val	Leu	Glu	Ala	Thr	Ala	
		595					600					605				
GTT	ATA	AAA	ACT	GGT	ACT	TGT	CCT	TTC	TCA	TTT	GAT	AAA	TTG	AAC	AAT	1872
Val	Ile	Lys	Thr	Gly	Thr	Cys	Pro	Phe	Ser	Phe	Asp	Lys	Leu	Asn	Asn	
	610					615					620					
TAC	TTG	ACT	TTT	AAC	AAG	TTC	TGT	TTG	TCG	TTG	AGT	CCT	GTT	GGT	GCT	1920
Tyr	Leu	Thr	Phe	Asn	Lys	Phe	Cys	Leu	Ser	Leu	Ser	Pro	Val	Gly	Ala	
625					630					635					640	
AAT	TGC	AAG	TTT	GAT	GTT	GCT	GCA	CGT	ACA	AGA	ACC	AAT	GAG	CAG	GTT	1968
Asn	Cys	Lys	Phe	Asp	Val	Ala	Ala	Arg	Thr	Arg	Thr	Asn	Glu	Gln	Val	
				645					650					655		
GTT	AGA	AGT	CTA	TAT	GTA	ATA	TAT	GAA	GAA	GGA	GAC	AAC	ATA	GTG	GGT	2016
Val	Arg	Ser	Leu	Tyr	Val	Ile	Tyr	Glu	Glu	Gly	Asp	Asn	Ile	Val	Gly	
			660					665					670			
GTA	CCG	TCT	GAT	AAT	AGC	GGT	CTG	CAC	GAT	TTG	TCT	GTG	CTA	CAC	CTA	2064
Val	Pro	Ser	Asp	Asn	Ser	Gly	Leu	His	Asp	Leu	Ser	Val	Leu	His	Leu	
			675				680					685				
GAC	TCC	TGT	ACA	GAT	TAC	AAT	ATA	TAT	GGT	AGA	ACT	GGT	GTT	GGT	ATT	2112
Asp	Ser	Cys	Thr	Asp	Tyr	Asn	Ile	Tyr	Gly	Arg	Thr	Gly	Val	Gly	Ile	
	690					695					700					
ATT	AGA	CGA	ACT	AAC	AGT	ACG	CTA	CTT	AGT	GGC	TTA	TAT	TAC	ACA	TCA	2160
Ile	Arg	Arg	Thr	Asn	Ser	Thr	Leu	Leu	Ser	Gly	Leu	Tyr	Tyr	Thr	Ser	
705					710					715					720	
CTA	TCA	GGT	GAT	TTG	TTA	GGC	TTT	AAA	AAT	GTT	AGT	GAT	GGT	GTC	ATT	2208
Leu	Ser	Gly	Asp	Leu	Leu	Gly	Phe	Lys	Asn	Val	Ser	Asp	Gly	Val	Ile	
				725					730					735		
TAT	TCT	GTG	ACG	CCA	TGT	GAT	GTA	AGC	GCA	CAA	GCG	GCT	GTT	ATT	GAT	2256
Tyr	Ser	Val	Thr	Pro	Cys	Asp	Val	Ser	Ala	Gln	Ala	Ala	Val	Ile	Asp	
			740					745					750			
GGT	GCC	ATA	GTT	GGA	GCT	ATG	ACT	TCC	ATT	AAC	AGT	GAA	CTG	TTA	GGT	2304
Gly	Ala	Ile	Val	Gly	Ala	Met	Thr	Ser	Ile	Asn	Ser	Glu	Leu	Leu	Gly	
		755					760					765				
CTA	ACA	CAT	TGG	ACA	ACG	ACA	CCT	AAT	TTT	TAT	TAC	TAC	TCT	ATA	TAT	2352
Leu	Thr	His	Trp	Thr	Thr	Thr	Pro	Asn	Phe	Tyr	Tyr	Tyr	Ser	Ile	Tyr	
	770					775					780					
AAT	TAC	ACA	AGT	GAG	AGG	ACT	CGT	GGC	ACT	GCA	ATT	GAC	AGT	AAC	GAT	2400
Asn	Tyr	Thr	Ser	Glu	Arg	Thr	Arg	Gly	Thr	Ala	Ile	Asp	Ser	Asn	Asp	
785					790					795					800	

GTT	GAT	TGT	GAA	CCT	GTC	ATA	ACC	TAT	TCT	AAT	ATA	GGT	GTT	TGT	AAA	2448
Val	Asp	Cys	Glu	Pro	Val	Ile	Thr	Tyr	Ser	Asn	Ile	Gly	Val	Cys	Lys	
				805					810					815		
AAT	GGT	GCT	TTG	GTT	TTT	ATT	AAC	GTC	ACA	CAT	TCT	GAC	GGA	GAC	GTG	2496
Asn	Gly	Ala	Leu	Val	Phe	Ile	Asn	Val	Thr	His	Ser	Asp	Gly	Asp	Val	
			820					825					830			
CAA	CCA	ATT	AGC	ACT	GGT	AAT	GTC	ACG	ATA	CCT	ACA	AAT	TTT	ACC	ATA	2544
Gln	Pro	Ile	Ser	Thr	Gly	Asn	Val	Thr	Ile	Pro	Thr	Asn	Phe	Thr	Ile	
			835				840					845				
TCT	GTG	CAA	GTT	GAA	TAC	ATG	CAG	GTT	TAC	ACT	ACA	CCA	GTA	TCA	ATA	2592
Ser	Val	Gln	Val	Glu	Tyr	Met	Gln	Val	Tyr	Thr	Thr	Pro	Val	Ser	Ile	
	850					855				860						
GAT	TGT	GCA	AGA	TAC	GTT	TGT	AAT	GGT	AAC	CCT	AGA	TGT	AAC	AAA	TTG	2640
Asp	Cys	Ala	Arg	Tyr	Val	Cys	Asn	Gly	Asn	Pro	Arg	Cys	Asn	Lys	Leu	
					870					875				880		
TTA	ACA	CAA	TAT	GTG	TCT	GCA	TGT	CAA	ACT	ATT	GAA	CAA	GCA	CTT	GCA	2688
Leu	Thr	Gln	Tyr	Val	Ser	Ala	Cys	Gln	Thr	Ile	Glu	Gln	Ala	Leu	Ala	
				885					890					895		
ATG	GGT	GCC	AGA	CTT	GAA	AAC	ATG	GAG	GTT	GAT	TCC	ATG	TTG	TTT	GTC	2736
Met	Gly	Ala	Arg	Leu	Glu	Asn	Met	Glu	Val	Asp	Ser	Met	Leu	Phe	Val	
			900					905					910			
TCG	GAA	AAT	GCC	CTT	AAA	TTG	GCA	TCT	GTT	GAG	GCG	TTC	AAT	AGT	ACA	2784
Ser	Glu	Asn	Ala	Leu	Lys	Leu	Ala	Ser	Val	Glu	Ala	Phe	Asn	Ser	Thr	
			915				920					925				
GAA	AAT	TTA	GAT	CCT	ATT	TAC	AAA	GAA	TGG	CCT	AGC	ATA	GGT	GGT	TCT	2832
Glu	Asn	Leu	Asp	Pro	Ile	Tyr	Lys	Glu	Trp	Pro	Ser	Ile	Gly	Gly	Ser	
			930			935					940					
TGG	CTA	GGA	GGT	CTA	AAA	GAT	ATA	CTA	CCG	TCC	CAT	AAT	AGC	AAA	CGT	2880
Trp	Leu	Gly	Gly	Leu	Lys	Asp	Ile	Leu	Pro	Ser	His	Asn	Ser	Lys	Arg	
	945				950				955					960		
AAG	TAT	GGT	TCT	GCT	ATA	GAA	GAT	TTG	CTT	TTT	GAT	AAA	GTT	GTA	ACA	2928
Lys	Tyr	Gly	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp	Lys	Val	Val	Thr	
				965				970						975		
TCT	GGT	TTA	GGT	ACA	GTT	GAT	GAA	GAT	TAT	AAA	CGT	TGT	ACT	GGT	GGT	2976
Ser	Gly	Leu	Gly	Thr	Val	Asp	Glu	Asp	Tyr	Lys	Arg	Cys	Thr	Gly	Gly	
			980				985					990				
TAC	GAC	ATA	GCA	GAC	TTG	GTG	TGT	GCT	CAA	TAT	TAC	AAT	GGC	ATC	ATG	3024
Tyr	Asp	Ile	Ala	Asp	Leu	Val	Cys	Ala	Gln	Tyr	Tyr	Asn	Gly	Ile	Met	
			995				1000					1005				
GTT	CTA	CCA	GGT	GTA	GCT	AAT	GCT	GAC	AAG	ATG	ACT	ATG	TAC	ACA	GCA	3072
Val	Leu	Pro	Gly	Val	Ala	Asn	Ala	Asp	Lys	Met	Thr	Met	Tyr	Thr	Ala	
	1010				1015						1020					
TCA	CTT	GCA	GGT	GGT	ATA	ACA	TTA	GGT	GCA	CTT	GGT	GGT	GGC	GCC	GTG	3120
Ser	Leu	Ala	Gly	Gly	Ile	Thr	Leu	Gly	Ala	Leu	Gly	Gly	Gly	Ala	Val	
	1025				1030				1035					1040		
GCT	ATA	CCT	TTT	GCA	GTA	GCA	GTA	CAG	GCT	AGA	CTT	AAT	TAT	GTT	GCT	3168
Ala	Ile	Pro	Phe	Ala	Val	Ala	Val	Gln	Ala	Arg	Leu	Asn	Tyr	Val	Ala	
				1045				1050					1055			
CTA	CAA	ACT	GAT	GTA	TTG	AAT	AAA	AAC	CAA	CAG	ATC	CTG	GCT	AAT	GCT	3216
Leu	Gln	Thr	Asp	Val	Leu	Asn	Lys	Asn	Gln	Gln	Ile	Leu	Ala	Asn	Ala	
			1060				1065					1070				

TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744
ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340	4032

TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT ACC ATT AAT Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn 1365 1370 1375	4128
AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT CTA GTA GTA GTA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe 1395 1400 1405	4224
TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA TAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
TAA	4365

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45
Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60
Trp Tyr Asn Cys Ser Arg Thr Ala Gln Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125



Gln	Arg	Pro	Leu	Leu	Lys	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	
	130					135					140					
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	
145					150					155					160	
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	
				165					170					175		
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	
			180					185					190			
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	
		195					200					205				
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235					240	
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	
				245					250					255		
Tyr	Glu	His	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Ser	
			260					265					270			
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu	
		275					280					285				
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro	
	290					295					300					
Leu	Leu	Ile	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Ala	Ala	
305					310					315					320	
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Asn	Gly	Val	
				325					330					335		
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr	
			340					345					350			
Ala	Asp	Val	Gln	Ser	Gly	Met	Gly	Ala	Thr	Val	Phe	Ser	Leu	Asn	Thr	
		355					360					365				
Thr	Gly	Gly	Val	Ile	Leu	Glu	Ile	Ser	Cys	Tyr	Ser	Asp	Thr	Val	Ser	
	370					375					380					
Glu	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Glu	Ile	Pro	Phe	Gly	Ile	Thr	Asp	
385					390					395					400	
Gly	Pro	Arg	Tyr	Cys	Tyr	Val	Leu	Tyr	Asn	Gly	Thr	Ala	Leu	Lys	Tyr	
				405					410					415		
Leu	Gly	Thr	Leu	Pro	Pro	Ser	Val	Lys	Glu	Ile	Ala	Ile	Ser	Lys	Trp	
			420					425					430			
Gly	His	Phe	Tyr	Ile	Asn	Gly	Tyr	Asn	Phe	Phe	Ser	Thr	Phe	Pro	Ile	
		435					440					445				
Gly	Cys	Ile	Ser	Phe	Asn	Leu	Thr	Thr	Gly	Ala	Ser	Gly	Ala	Phe	Trp	
	450					455					460					
Thr	Ile	Ala	Tyr	Thr	Ser	Tyr	Thr	Glu	Ala	Leu	Val	Gln	Val	Glu	Asn	
465					470					475					480	

Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
 485 490 495  
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
 500 505 510  
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
 515 520 525  
 Ser Phe Phe Thr His Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
 530 535 540  
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
 545 550 555 560  
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
 565 570 575  
 Asn Gln Phe Ser Val Tyr Val Pro Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590  
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700  
 Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720  
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735  
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp  
 740 745 750  
 Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly  
 755 760 765  
 Leu Thr His Trp Thr Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr  
 770 775 780  
 Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp  
 785 790 795 800  
 Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys  
 805 810 815  
 Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val  
 820 825 830

Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile  
 835 840 845  
 Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Thr Pro Val Ser Ile  
 850 855 860  
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu  
 865 870 875 880  
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala  
 885 890 895  
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val  
 900 905 910  
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr  
 915 920 925  
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser  
 930 935 940  
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg  
 945 950 955 960  
 Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr  
 965 970 975  
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly  
 980 985 990  
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met  
 995 1000 1005  
 Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala  
 1010 1015 1020  
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val  
 1025 1030 1035 1040  
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala  
 1045 1050 1055  
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070  
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085  
 Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100  
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120  
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135  
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150  
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165  
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180



Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe  
 1185 1190 1195 1200  
 Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala  
 1205 1210 1215  
 Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr  
 1220 1225 1230  
 Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg  
 1235 1240 1245  
 Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn  
 1250 1255 1260  
 Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg  
 1265 1270 1275 1280  
 Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu  
 1285 1290 1295  
 Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr  
 1300 1305 1310  
 Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro  
 1315 1320 1325  
 Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr  
 1330 1335 1340  
 Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys  
 1345 1350 1355 1360  
 Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn  
 1365 1370 1375  
 Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val  
 1380 1385 1390  
 Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe  
 1395 1400 1405  
 Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly  
 1410 1415 1420  
 Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg  
 1425 1430 1435 1440  
 Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His  
 1445 1450

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2244

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG	ATT	GTG	CTC	GTA	ACT	TGC	CTC	TTG	TTG	TTA	TGT	TCA	TAC	CAC	ACA	48
Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr	
1				5				10						15		
GTT	TTG	AGT	ACA	ACA	AAT	AAT	GAA	TGC	ATA	CAA	GTT	AAC	GTA	ACA	CAA	96
Val	Leu	Ser	Thr	Thr	Asn	Asn	Glu	Cys	Ile	Gln	Val	Asn	Val	Thr	Gln	
			20				25						30			
TTG	GCT	GGC	AAT	GAA	AAC	CTT	ATC	AGA	GAT	TTT	CTG	TTT	AGT	AAC	TTT	144
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Ser	Asn	Phe	
		35					40					45				
AAA	GAA	GAA	GGA	AGT	GTA	GTT	GTT	GGT	GGT	TAT	TAC	CCT	ACA	GAG	GTG	192
Lys	Glu	Glu	Gly	Ser	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val	
	50					55					60					
TGG	TAC	AAC	TGC	TCT	AGA	ACA	GCT	CGA	ACT	ACT	GCC	TTT	CAG	TAT	TTT	240
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Arg	Thr	Thr	Ala	Phe	Gln	Tyr	Phe	
65					70					75					80	
AAT	AAT	ATA	CAT	GCC	TTT	TAT	TTT	GTT	ATG	GAA	GCC	ATG	GAA	AAT	AGC	288
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Val	Met	Glu	Ala	Met	Glu	Asn	Ser	
				85					90					95		
ACT	GGT	AAT	GCA	CGT	GGT	AAA	CCA	TTA	TTA	TTT	CAT	GTG	CAT	GGT	GAG	336
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu	
			100					105					110			
CCT	GTT	AGT	GTT	ATT	ATA	TAT	ATA	TCG	GCT	TAT	AGG	GAT	GAT	GTG	CAA	384
Pro	Val	Ser	Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln	
		115				120					125					
CAA	AGG	CCC	CTT	TTA	GAA	CAT	GGG	TTA	GTG	TGC	ATA	ACT	AAA	AAT	CGC	432
Gln	Arg	Pro	Leu	Leu	Glu	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	
	130					135					140					
CAT	ATT	AAC	TAT	GAA	CAA	TTC	ACC	TCC	AAC	CAG	TGG	AAT	TCC	ACA	TGT	480
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	
145					150					155					160	
ACG	GGT	GCT	GAC	AGA	AAA	ATT	CCT	TTC	TCT	GTC	ATA	CCC	ACG	GAC	AAT	528
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	
				165					170					175		
GGA	ACA	AAA	ATC	TAT	GGT	CTT	GAG	TGG	AAT	GAT	GAC	TTT	GTT	ACA	GCT	576
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	
		180						185					190			
TAT	ATT	AGT	GGT	CGT	TCT	TAT	CAC	TTG	AAC	ATC	AAT	ACT	AAT	TGG	TTT	624
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	
		195					200					205				
AAC	AAT	GTC	ACA	CTT	TTG	TAT	TCA	CGC	TCA	AGC	ACT	GCT	ACC	TGG	GAA	672
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
TAC	AGT	GCT	GCA	TAT	GCT	TAC	CAA	GGT	GTT	TCT	AAC	TTC	ACT	TAT	TAC	720
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235					240	
AAG	TTA	AAT	AAC	ACC	AAT	GGT	CTA	AAA	ACC	TAT	GAA	TTA	TGT	GAA	GAT	768
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	
				245					250					255		

TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270	816
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCC ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

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AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATC TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112
ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala 740 745	2246

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr	1	5	10	15
Val	Leu	Ser	Thr	Thr	Asn	Asn	Glu	Cys	Ile	Gln	Val	Asn	Val	Thr	Gln	20	25	30	
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Ser	Asn	Phe	35	40	45	
Lys	Glu	Glu	Gly	Ser	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val	50	55	60	
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Arg	Thr	Thr	Ala	Phe	Gln	Tyr	Phe	65	70	75	80
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Val	Met	Glu	Ala	Met	Glu	Asn	Ser	85	90	95	
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu	100	105	110	
Pro	Val	Ser	Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln	115	120	125	
Gln	Arg	Pro	Leu	Leu	Glu	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	130	135	140	
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	145	150	155	160
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	165	170	175	
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	180	185	190	
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	195	200	205	
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	210	215	220	
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	225	230	235	240
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	245	250	255	
Tyr	Glu	His	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Ser	260	265	270	
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu	275	280	285	
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro	290	295	300	
Leu	Leu	Ile	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Ala	Ala	305	310	315	320
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Asn	Gly	Val	325	330	335	
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr	340	345	350	

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Ala	Asp	Val	Gln	Ser	Gly	Met	Gly	Ala	Thr	Val	Phe	Ser	Leu	Asn	Thr
		355					360					365			
Thr	Gly	Gly	Val	Ile	Leu	Glu	Ile	Ser	Cys	Tyr	Ser	Asp	Thr	Val	Ser
	370					375					380				
Glu	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Glu	Ile	Pro	Phe	Gly	Ile	Thr	Asp
385					390					395					400
Gly	Pro	Arg	Tyr	Cys	Tyr	Val	Leu	Tyr	Asn	Gly	Thr	Ala	Leu	Lys	Tyr
				405					410					415	
Leu	Gly	Thr	Leu	Pro	Pro	Ser	Val	Lys	Glu	Ile	Ala	Ile	Ser	Lys	Trp
			420					425					430		
Gly	His	Phe	Tyr	Ile	Asn	Gly	Tyr	Asn	Phe	Phe	Ser	Thr	Phe	Pro	Ile
		435					440					445			
Gly	Cys	Ile	Ser	Phe	Asn	Leu	Thr	Thr	Gly	Val	Ser	Gly	Ala	Phe	Trp
	450					455					460				
Thr	Ile	Ala	Tyr	Thr	Ser	Tyr	Thr	Glu	Ala	Leu	Val	Gln	Val	Glu	Asn
465					470					475					480
Thr	Ala	Ile	Lys	Asn	Val	Thr	Tyr	Cys	Asn	Ser	His	Ile	Asn	Asn	Ile
				485					490					495	
Lys	Cys	Ser	Gln	Leu	Thr	Ala	Asn	Leu	Asn	Asn	Gly	Phe	Tyr	Pro	Val
			500					505					510		
Ala	Ser	Ser	Glu	Val	Gly	Phe	Val	Asn	Lys	Ser	Val	Val	Leu	Leu	Pro
		515					520					525			
Ser	Phe	Phe	Thr	Tyr	Thr	Ala	Val	Asn	Ile	Thr	Ile	Asp	Leu	Gly	Met
	530					535					540				
Lys	Leu	Ser	Gly	Tyr	Gly	Gln	Pro	Ile	Ala	Ser	Thr	Leu	Ser	Asn	Ile
545					550					555					560
Thr	Leu	Pro	Met	Gln	Asp	Asn	Asn	Thr	Asp	Val	Tyr	Cys	Ile	Arg	Ser
				565					570					575	
Asn	Gln	Phe	Ser	Val	Tyr	Val	His	Ser	Thr	Cys	Lys	Ser	Ser	Leu	Trp
			580					585					590		
Asp	Asn	Ile	Phe	Asn	Gln	Asp	Cys	Thr	Asp	Val	Leu	Glu	Ala	Thr	Ala
		595					600					605			
Val	Ile	Lys	Thr	Gly	Thr	Cys	Pro	Phe	Ser	Phe	Asp	Lys	Leu	Asn	Asn
	610					615					620				
Tyr	Leu	Thr	Phe	Asn	Lys	Phe	Cys	Leu	Ser	Leu	Ser	Pro	Val	Gly	Ala
625					630					635					640
Asn	Cys	Lys	Phe	Asp	Val	Ala	Ala	Arg	Thr	Arg	Thr	Asn	Glu	Gln	Val
				645					650					655	
Val	Arg	Ser	Leu	Tyr	Val	Ile	Tyr	Glu	Glu	Gly	Asp	Asn	Ile	Val	Gly
			660					665					670		
Val	Pro	Ser	Asp	Asp	Ser	Gly	Leu	His	Asp	Leu	Ser	Val	Leu	His	Leu
		675					680					685			
Asp	Ser	Cys	Thr	Asp	Tyr	Asn	Ile	Tyr	Gly	Arg	Thr	Gly	Val	Gly	Ile
		690				695					700				



Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA	48
Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr	
1 5 10 15	
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTT ACA CAA	96
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln	
20 25 30	
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT	144
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe	
35 40 45	
AAA GAA GAA GGA AGT GTA GTT GTT GGT GGT TAT TAC CCT ACA GAG GTG	192
Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val	
50 55 60	
TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT	240
Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe	
65 70 75 80	
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC	288
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser	
85 90 95	
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG	336
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu	
100 105 110	
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA	384
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln	
115 120 125	
CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC	432
Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg	
130 135 140	
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT	480
His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys	
145 150 155 160	

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ACG	GGT	GCT	GAC	AGA	AAA	ATT	CCT	TTC	TCT	GTC	ATA	CCC	ACG	GAC	AAT	528
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	
				165					170					175		
GGA	ACA	AAA	ATC	TAT	GGT	CTT	GAG	TGG	AAT	GAT	GAC	TTT	GTT	ACA	GCT	576
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	
			180					185					190			
TAT	ATT	AGT	GGT	CGT	TCT	TAT	CAC	TTG	AAC	ATC	AAT	ACT	AAT	TGG	TTT	624
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	
		195					200					205				
AAC	AAT	GTC	ACA	CTT	TTG	TAT	TCA	CGC	TCA	AGC	ACT	GCT	ACC	TGG	GAA	672
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
TAC	AGT	GCT	GCA	TAT	GCT	TAC	CAA	GGT	GTT	TCT	AAC	TTC	ACT	TAT	TAC	720
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235				240		
AAG	TTA	AAT	AAC	ACC	AAT	GGT	CTA	AAA	ACC	TAT	GAA	TTA	TGT	GAA	GAT	768
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	
				245					250					255		
TAT	GAA	CAT	TGC	ACT	GGC	TAT	GCT	ACC	AAT	GTA	TTT	GCT	CCG	ACA	TCA	816
Tyr	Glu	His	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Ser	
			260					265					270			
GGT	GGT	TAC	ATA	CCT	GAT	GGA	TTT	AGT	TTT	AAT	AAT	TGG	TTC	TTG	CTT	864
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu	
		275					280					285				
ACA	AAT	AGT	TCC	ACT	TTT	GTT	AGT	GGC	AGG	TTT	GTA	ACA	AAT	CAA	CCA	912
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro	
	290					295					300					
TTA	TTG	ATT	AAT	TGC	TTG	TGG	CCA	GTG	CCC	AGT	TTT	GGT	GTA	GTA	GCA	960
Leu	Leu	Ile	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Val	Ala	
305					310					315					320	
CAA	GAA	TTT	TGT	TTT	GAA	GGT	GCA	CAG	TTT	AGC	CAA	TGT	AAT	GGT	GTG	1008
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Asn	Gly	Val	
				325					330					335		
TCT	TTA	AAT	AAC	ACA	GTG	GAT	GTT	ATT	AGA	TTC	AAC	CTT	AAT	TTC	ACT	1056
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr	
			340					345					350			
GCA	GAT	GTA	CAA	TCT	GGT	ATG	GGT	GCT	ACA	GTA	TTT	TCA	CTG	AAT	ACA	1104
Ala	Asp	Val	Gln	Ser	Gly	Met	Gly	Ala	Thr	Val	Phe	Ser	Leu	Asn	Thr	
		355					360					365				
ACA	GGT	GGT	GTC	ATT	CTT	GAA	ATT	TCA	TGT	TAT	AGT	GAC	ACA	GTG	AGT	1152
Thr	Gly	Gly	Val	Ile	Leu	Glu	Ile	Ser	Cys	Tyr	Ser	Asp	Thr	Val	Ser	
	370					375					380					
GAG	TCT	AGT	TCT	TAC	AGT	TAT	GGT	GAA	ATC	CCG	TTC	GGC	ATA	ACT	GAC	1200
Glu	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Glu	Ile	Pro	Phe	Gly	Ile	Thr	Asp	
385					390					395					400	
GGA	CCA	CGA	TAC	TGT	TAT	GTA	CTT	TAC	AAT	GGC	ACA	GCT	CTT	AAA	TAT	1248
Gly	Pro	Arg	Tyr	Cys	Tyr	Val	Leu	Tyr	Asn	Gly	Thr	Ala	Leu	Lys	Tyr	
				405					410					415		
TTA	GGA	ACA	TTA	CCA	CCC	AGT	GTA	AAG	GAA	ATT	GCT	ATT	AGT	AAG	TGG	1296
Leu	Gly	Thr	Leu	Pro	Pro	Ser	Val	Lys	Glu	Ile	Ala	Ile	Ser	Lys	Trp	
			420					425							430	



GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584
AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC ACG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT ATA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112

ATT Ile 705	AGA Arg	CGA Arg	ACT Thr	AAC Asn	AGT Ser 710	ACG Thr	CTA Leu	CTT Leu	AGT Ser	GGC Gly 715	TTA Leu	TAT Tyr	TAC Tyr	ACA Thr	TCA Ser 720	2160
CTA Leu	TCA Ser	GGT Gly	GAT Asp	TTG Leu 725	TTA Leu	GGC Gly	TTT Phe	AAA Lys	AAT Asn 730	GTT Val	AGT Ser	GAT Asp	GGT Gly	GTC Val 735	ATT Ile	2208
TAT Tyr	TCT Ser	GTG Val	ACG Thr 740	CCA Pro	TGT Cys	GAT Asp	GTA Val	AGC Ser 745	GCA Ala	CAA Gln	GCG Ala	GCT Ala	GTT Val 750	ATT Ile	GAT Asp	2256
GGT Gly	GCC Ala	ATA Ile 755	GTT Val	GGA Gly	GCT Ala	ATG Met	ACT Thr 760	TCC Ser	ATT Ile	AAC Asn	AGT Ser	GAA Glu 765	CTG Leu	TTA Leu	GGT Gly	2304
CTA Leu 770	ATA Ile	CAT His	TGG Trp	ACA Thr	ACG Thr	ACA Thr 775	CCT Pro	AAT Asn	TTT Phe	TAT Tyr 780	TAC Tyr	TAC Tyr	TCT Ser	ATA Ile	TAT Tyr	2352
AAT Asn 785	TAC Tyr	ACA Thr	AGT Ser	GAG Glu	AGG Arg 790	ACT Thr	CGT Arg	GGC Gly	ACT Thr	GCA Ala 795	ATT Ile	GAC Asp	AGT Ser	AAC Asn	GAT Asp 800	2400
GTT Val	GAT Asp	TGT Cys	GAA Glu	CCT Pro 805	GTC Val	ATA Ile	ACC Thr	TAT Tyr	TCT Ser	AAT Asn 810	ATA Ile	GGT Gly	GTT Val	TGT Cys 815	AAA Lys	2448
AAT Asn	GGT Gly	GCT Ala	TTG Leu 820	GTT Val	TTT Phe	ATT Ile	AAC Asn	GTC Val 825	ACA Thr	CAT His	TCT Ser	GAC Asp	GGA Gly 830	GAC Asp	GTG Val	2496
CAA Gln	CCA Pro	ATT Ile 835	AGC Ser	ACT Thr	GGT Gly	AAT Asn	GTC Val 840	ACG Thr	ATA Ile	CCT Pro	ACA Thr	AAT Asn 845	TTT Phe	ACC Thr	ATA Ile	2544
TCT Ser 850	GTG Val	CAA Gln	GTT Val	GAA Glu	TAC Tyr	ATG Met 855	CAG Gln	GTT Val	TAC Tyr	ACT Thr	ACA Thr 860	CCA Pro	GTA Val	TCA Ser	ATA Ile	2592
GAT Asp 865	TGT Cys	GCA Ala	AGA Arg	TAC Tyr	GTT Val 870	TGT Cys	AAT Asn	GGT Gly	AAC Asn	CCT Pro 875	AGA Arg	TGT Cys	AAC Asn	AAA Lys	TTG Leu 880	2640
TTA Leu	ACA Thr	CAA Gln	TAT Tyr	GTG Val 885	TCT Ser	GCA Ala	TGT Cys	CAA Gln	ACT Thr 890	ATT Ile	GAA Glu	CAA Gln	GCA Ala	CTT Leu 895	GCA Ala	2688
ATG Met	GGT Gly	GCC Ala	AGA Arg 900	CTT Leu	GAA Glu	AAC Asn	ATG Met	GAG Glu	GTT Val	GAT Asp	TCC Ser	ATG Met	TTG Leu 910	TTT Phe	GTC Val	2736
TCG Ser	GAA Glu	AAT Asn 915	GCC Ala	CTT Leu	AAA Lys	TTG Leu	GCA Ala 920	TCT Ser	GTT Val	GAG Glu	GCG Ala	TTC Phe 925	AAT Asn	AGT Ser	ACA Thr	2784
GAA Glu 930	AAT Asn	TTA Leu	GAT Asp	CCT Pro	ATT Ile	TAC Tyr 935	AAA Lys	GAA Glu	TGG Trp	CCT Pro	AGC Ser 940	ATA Ile	GGT Gly	GGT Gly	TCT Ser	2832
TGG Trp 945	CTA Leu	GGA Gly	GGT Gly	CTA Leu	AAA Lys 950	GAT Asp	ATA Ile	CTA Leu	CCG Pro	TCC Ser 955	CAT His	AAT Asn	AGC Ser	AAA Lys	CGT Arg 960	2880
AAG Lys	TAT Tyr	GGT Gly	TCT Ser	GCT Ala 965	ATA Ile	GAA Glu	GAT Asp	TTG Leu	CTT Leu 970	TTT Phe	GAT Asp	AAA Lys	GTT Val	GTA Val 975	ACA Thr	2928

TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACT GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990	2976
TAC GAC ATA GCA GAC TTG GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005	3024
GTT CTA CCA GGT GTA GCT AAT GCT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020	3072
TCA CTT GCA GGT GGT ATA ACA TTA GGT GCA CTT GGT GGT GGC GCC GTG Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val 1025 1030 1035 1040	3120
GCT ATA CCT TTT GCA GTA GCA GTA CAG GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055	3168
CTA CAA ACT GAT GTA TTG AAT AAA AAC CAA CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070	3216
TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744

ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC ACA ACC TAT Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr 1330 1335 1340	4032
TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCG GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT AAC ATT AAT Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn 1365 1370 1375	4128
AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT TTA GTA GTA GTA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe 1395 1400 1405	4224
TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
TAA	4365

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr	1	5	10	15
Val	Leu	Ser	Thr	Thr	Asn	Asn	Glu	Cys	Ile	Gln	Val	Asn	Val	Thr	Gln	20	25	30	
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Ser	Asn	Phe	35	40	45	
Lys	Glu	Glu	Gly	Ser	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val	50	55	60	
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Arg	Thr	Thr	Ala	Phe	Gln	Tyr	Phe	65	70	75	80
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Val	Met	Glu	Ala	Met	Glu	Asn	Ser	85	90	95	
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu	100	105	110	
Pro	Val	Ser	Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln	115	120	125	
Gln	Arg	Pro	Leu	Leu	Lys	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	130	135	140	
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	145	150	155	160
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	165	170	175	
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	180	185	190	
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	195	200	205	
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	210	215	220	
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	225	230	235	240
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	245	250	255	
Tyr	Glu	His	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Ser	260	265	270	
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu	275	280	285	
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro	290	295	300	
Leu	Leu	Ile	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Val	Ala	305	310	315	320
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Asn	Gly	Val	325	330	335	
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr	340	345	350	



Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
 355 360 365  
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
 370 375 380  
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
 385 390 395 400  
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
 405 410 415  
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
 420 425 430  
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
 435 440 445  
 Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
 450 455 460  
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
 465 470 475 480  
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
 485 490 495  
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
 500 505 510  
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
 515 520 525  
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
 530 535 540  
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
 545 550 555 560  
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
 565 570 575  
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590  
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700

111

Ile 705	Arg	Arg	Thr	Asn	Ser 710	Thr	Leu	Leu	Ser	Gly 715	Leu	Tyr	Tyr	Thr	Ser 720
Leu	Ser	Gly	Asp	Leu 725	Leu	Gly	Phe	Lys	Asn 730	Val	Ser	Asp	Gly	Val 735	Ile
Tyr	Ser	Val	Thr 740	Pro	Cys	Asp	Val	Ser 745	Ala	Gln	Ala	Ala	Val 750	Ile	Asp
Gly	Ala	Ile 755	Val	Gly	Ala	Met	Thr 760	Ser	Ile	Asn	Ser	Glu 765	Leu	Leu	Gly
Leu 770	Ile	His	Trp	Thr	Thr	Thr 775	Pro	Asn	Phe	Tyr	Tyr 780	Tyr	Ser	Ile	Tyr
Asn 785	Tyr	Thr	Ser	Glu	Arg 790	Thr	Arg	Gly	Thr	Ala 795	Ile	Asp	Ser	Asn	Asp 800
Val	Asp	Cys	Glu	Pro 805	Val	Ile	Thr	Tyr	Ser 810	Asn	Ile	Gly	Val	Cys 815	Lys
Asn	Gly	Ala	Leu 820	Val	Phe	Ile	Asn 825	Val	Thr	His	Ser	Asp	Gly 830	Asp	Val
Gln	Pro	Ile 835	Ser	Thr	Gly	Asn	Val 840	Thr	Ile	Pro	Thr	Asn 845	Phe	Thr	Ile
Ser 850	Val	Gln	Val	Glu	Tyr	Met 855	Gln	Val	Tyr	Thr	Thr 860	Pro	Val	Ser	Ile
Asp 865	Cys	Ala	Arg	Tyr	Val 870	Cys	Asn	Gly	Asn	Pro 875	Arg	Cys	Asn	Lys	Leu 880
Leu	Thr	Gln	Tyr	Val 885	Ser	Ala	Cys	Gln	Thr 890	Ile	Glu	Gln	Ala	Leu 895	Ala
Met	Gly	Ala	Arg 900	Leu	Glu	Asn	Met	Glu 905	Val	Asp	Ser	Met	Leu 910	Phe	Val
Ser	Glu	Asn 915	Ala	Leu	Lys	Leu	Ala 920	Ser	Val	Glu	Ala	Phe 925	Asn	Ser	Thr
Glu 930	Asn	Leu	Asp	Pro	Ile	Tyr 935	Lys	Glu	Trp	Pro	Ser 940	Ile	Gly	Gly	Ser
Trp 945	Leu	Gly	Gly	Leu	Lys 950	Asp	Ile	Leu	Pro	Ser 955	His	Asn	Ser	Lys	Arg 960
Lys	Tyr	Gly	Ser	Ala 965	Ile	Glu	Asp	Leu	Leu 970	Phe	Asp	Lys	Val	Val 975	Thr
Ser	Gly	Leu	Gly 980	Thr	Val	Asp	Glu	Asp 985	Tyr	Lys	Arg	Cys	Thr 990	Gly	Gly
Tyr	Asp	Ile 995	Ala	Asp	Leu	Val	Cys 1000	Ala	Gln	Tyr	Tyr	Asn 1005	Gly	Ile	Met
Val 1010	Leu	Pro	Gly	Val	Ala	Asn 1015	Ala	Asp	Lys	Met	Thr 1020	Met	Tyr	Thr	Ala
Ser 1025	Leu	Ala	Gly	Gly	Ile 1030	Thr	Leu	Gly	Ala	Leu 1035	Gly	Gly	Gly	Ala	Val 1040
Ala	Ile	Pro	Phe	Ala	Val	Ala	Val	Gln 1045	Ala	Arg	Leu	Asn	Tyr	Val 1055	Ala

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Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070  
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085  
 Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100  
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120  
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135  
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150  
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165  
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180  
 Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe  
 1185 1190 1195 1200  
 Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala  
 1205 1210 1215  
 Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr  
 1220 1225 1230  
 Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg  
 1235 1240 1245  
 Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn  
 1250 1255 1260  
 Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg  
 1265 1270 1275 1280  
 Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu  
 1285 1290 1295  
 Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr  
 1300 1305 1310  
 Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro  
 1315 1320 1325  
 Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr  
 1330 1335 1340  
 Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys  
 1345 1350 1355 1360  
 Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn  
 1365 1370 1375  
 Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val  
 1380 1385 1390  
 Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe  
 1395 1400 1405



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Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly  
 1410 1415 1420

Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg  
 1425 1430 1435 1440

Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His  
 1445 1450

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2244

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA	48
Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr	
1 5 10 15	
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA	96
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln	
20 25 30	
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT	144
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe	
35 40 45	
AAA GAA GAA GGA AGT GTA GTT GTT GGT GGT TAT TAC CCT ACA GAG GTG	192
Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val	
50 55 60	
TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT	240
Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe	
65 70 75 80	
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC	288
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser	
85 90 95	
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG	336
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu	
100 105 110	
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA	384
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln	
115 120 125	
CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC	432
Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg	
130 135 140	
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT	480
His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys	
145 150 155 160	

ACG	GGT	GCT	GAC	AGA	AAA	ATT	CCT	TTC	TCT	GTC	ATA	CCC	ACG	GAC	AAT	528
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	
				165					170					175		
GGA	ACA	AAA	ATC	TAT	GGT	CTT	GAG	TGG	AAT	GAT	GAC	TTT	GTT	ACA	GCT	576
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	
			180					185					190			
TAT	ATT	AGT	GGT	CGT	TCT	TAT	CAC	TTG	AAC	ATC	AAT	ACT	AAT	TGG	TTT	624
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	
		195					200					205				
AAC	AAT	GTC	ACA	CTT	TTG	TAT	TCA	CGC	TCA	AGC	ACT	GCT	ACC	TGG	GAA	672
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
TAC	AGT	GCT	GCA	TAT	GCT	TAC	CAA	GGT	GTT	TCT	AAC	TTC	ACT	TAT	TAC	720
Tyr	Ser	Ala	Ala	Tyr	Ala	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235					240	
AAG	TTA	AAT	AAC	ACC	AAT	GGT	CTA	AAA	ACC	TAT	GAA	TTA	TGT	GAA	GAT	768
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Leu	Cys	Glu	Asp	
				245					250					255		
TAT	GAA	CAT	TGC	ACT	GGC	TAT	GCT	ACC	AAT	GTA	TTT	GCT	CCG	ACA	TCA	816
Tyr	Glu	His	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Ser	
			260					265					270			
GGT	GGT	TAC	ATA	CCT	GAT	GGA	TTT	AGT	TTT	AAT	AAT	TGG	TTC	TTG	CTT	864
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu	
		275					280					285				
ACA	AAT	AGT	TCC	ACT	TTT	GTT	AGT	GGC	AGG	TTT	GTA	ACA	AAT	CAA	CCA	912
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro	
	290					295					300					
TTA	TTG	ATT	AAT	TGC	TTG	TGG	CCA	GTG	CCC	AGT	TTT	GGT	GTA	GCA	GCA	960
Leu	Leu	Ile	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Ala	Ala	
305					310					315					320	
CAA	GAA	TTT	TGT	TTT	GAA	GGT	GCA	CAG	TTT	AGC	CAA	TGT	AAT	GGT	GTG	1008
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Asn	Gly	Val	
				325					330					335		
TCT	TTA	AAT	AAC	ACA	GTG	GAT	GTT	ATT	AGA	TTC	AAC	CTT	AAT	TTC	ACT	1056
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr	
			340					345					350			
GCA	GAT	GTA	CAA	TCT	GGT	ATG	GGT	GCT	ACA	GTA	TTT	TCA	CTG	AAT	ACA	1104
Ala	Asp	Val	Gln	Ser	Gly	Met	Gly	Ala	Thr	Val	Phe	Ser	Leu	Asn	Thr	
		355					360					365				
ACA	GGT	GGT	GTC	ATT	CTT	GAA	ATT	TCA	TGT	TAT	AGT	GAC	ACA	GTG	AGT	1152
Thr	Gly	Gly	Val	Ile	Leu	Glu	Ile	Ser	Cys	Tyr	Ser	Asp	Thr	Val	Ser	
	370					375					380					
GAG	TCT	AGT	TCT	TAC	AGT	TAT	GGT	GAA	ATC	CCG	TTC	GGC	ATA	ACT	GAC	1200
Glu	Ser	Ser	Ser	Tyr	Ser	Tyr	Gly	Glu	Ile	Pro	Phe	Gly	Ile	Thr	Asp	
385					390					395					400	
GGA	CCA	CGA	TAC	TGT	TAT	GTA	CTT	TAC	AAT	GGC	ACA	GCT	CTT	AAA	TAT	1248
Gly	Pro	Arg	Tyr	Cys	Tyr	Val	Leu	Tyr	Asn	Gly	Thr	Ala	Leu	Lys	Tyr	
				405					410					415		
TTA	GGA	ACA	TTA	CCA	CCC	AGT	GTA	AAG	GAA	ATT	GCT	ATT	AGT	AAG	TGG	1296
Leu	Gly	Thr	Leu	Pro	Pro	Ser	Val	Lys	Glu	Ile	Ala	Ile	Ser	Lys	Trp	
			420					425					430			

GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584
AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112

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ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA	2160
Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser	
705 710 715 720	
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT	2208
Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile	
725 730 735	
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC	2246
Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala	
740 745	

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr
1				5					10					15	
Val	Leu	Ser	Thr	Thr	Asn	Asn	Glu	Cys	Ile	Gln	Val	Asn	Val	Thr	Gln
			20					25					30		
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Ser	Asn	Phe
		35					40					45			
Lys	Glu	Glu	Gly	Ser	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val
	50					55					60				
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Arg	Thr	Thr	Ala	Phe	Gln	Tyr	Phe
65					70				75						80
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Val	Met	Glu	Ala	Met	Glu	Asn	Ser
				85					90					95	
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu
			100					105					110		
Pro	Val	Ser	Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln
			115				120					125			
Gln	Arg	Pro	Leu	Leu	Lys	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg
	130					135					140				
His	Ile	Asn	Tyr	Glu	Gln	Phe	Thr	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys
145					150					155					160
Thr	Gly	Ala	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn
			165						170					175	
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala
			180					185					190		
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe
		195					200					205			
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu
		210				215					220				

Tyr 225	Ser	Ala	Ala	Tyr	Ala 230	Tyr	Gln	Gly	Val	Ser 235	Asn	Phe	Thr	Tyr	Tyr 240
Lys	Leu	Asn	Asn	Thr 245	Asn	Gly	Leu	Lys	Thr 250	Tyr	Glu	Leu	Cys	Glu 255	Asp
Tyr	Glu	His	Cys 260	Thr	Gly	Tyr	Ala	Thr 265	Asn	Val	Phe	Ala	Pro 270	Thr	Ser
Gly	Gly	Tyr 275	Ile	Pro	Asp	Gly	Phe 280	Ser	Phe	Asn	Asn	Trp 285	Phe	Leu	Leu
Thr 290	Asn	Ser	Ser	Thr	Phe	Val 295	Ser	Gly	Arg	Phe	Val 300	Thr	Asn	Gln	Pro
Leu 305	Leu	Ile	Asn	Cys	Leu 310	Trp	Pro	Val	Pro	Ser 315	Phe	Gly	Val	Ala	Ala 320
Gln	Glu	Phe	Cys	Phe 325	Glu	Gly	Ala	Gln	Phe 330	Ser	Gln	Cys	Asn	Gly 335	Val
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile 345	Arg	Phe	Asn	Leu	Asn	Phe 350	Thr
Ala	Asp	Val 355	Gln	Ser	Gly	Met	Gly 360	Ala	Thr	Val	Phe	Ser 365	Leu	Asn	Thr
Thr 370	Gly	Gly	Val	Ile	Leu	Glu 375	Ile	Ser	Cys	Tyr	Ser 380	Asp	Thr	Val	Ser
Glu 385	Ser	Ser	Ser	Tyr	Ser 390	Tyr	Gly	Glu	Ile	Pro 395	Phe	Gly	Ile	Thr	Asp 400
Gly	Pro	Arg	Tyr	Cys 405	Tyr	Val	Leu	Tyr	Asn 410	Gly	Thr	Ala	Leu	Lys 415	Tyr
Leu	Gly	Thr 420	Leu	Pro	Pro	Ser	Val	Lys 425	Glu	Ile	Ala	Ile	Ser 430	Lys	Trp
Gly	His	Phe 435	Tyr	Ile	Asn	Gly	Tyr 440	Asn	Phe	Phe	Ser	Thr 445	Phe	Pro	Ile
Asp 450	Cys	Ile	Ser	Phe	Asn	Leu 455	Thr	Thr	Gly	Val	Ser 460	Gly	Ala	Phe	Trp
Thr 465	Ile	Ala	Tyr	Thr	Ser 470	Tyr	Thr	Glu	Ala	Leu 475	Val	Gln	Val	Glu	Asn 480
Thr	Ala	Ile	Lys	Asn 485	Val	Thr	Tyr	Cys	Asn 490	Ser	His	Ile	Asn	Asn 495	Ile
Lys	Cys	Ser	Gln 500	Leu	Thr	Ala	Asn	Leu 505	Asn	Asn	Gly	Phe	Tyr 510	Pro	Val
Ala	Ser	Ser 515	Glu	Val	Gly	Phe	Val 520	Asn	Lys	Ser	Val	Val 525	Leu	Leu	Pro
Ser 530	Phe	Phe	Thr	Tyr	Thr	Ala 535	Val	Asn	Ile	Thr	Ile 540	Asp	Leu	Gly	Met
Lys 545	Leu	Ser	Gly	Tyr	Gly 550	Gln	Pro	Ile	Ala	Ser 555	Thr	Leu	Ser	Asn	Ile 560
Thr	Leu	Pro	Met	Gln 565	Asp	Asn	Asn	Thr	Asp 570	Val	Tyr	Cys	Ile	Arg 575	Ser

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Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590  
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700  
 Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720  
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735  
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..368

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT GTT	47
Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val	
1 5 10 15	
ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC CTT	95
Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu	
20 25 30	
TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT AAC TAT	143
Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr	
35 40 45	
GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT GAC	191
Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp	
50 55 60	



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AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA ATC	239
Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile	
65 70 75	
TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT GGT	287
Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly	
80 85 90 95	
CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC ACA	335
Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr	
100 105 110	
CTT TTG TAT TCA CGC TCA AGC ATT GCT ACC TGG GA	370
Leu Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp	
115 120	

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val Ile	
1 5 10 15	
Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu Leu	
20 25 30	
Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr Glu	
35 40 45	
Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp Arg	
50 55 60	
Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile Tyr	
65 70 75 80	
Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly Arg	
85 90 95	
Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr Leu	
100 105 110	
Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp	
115 120	

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG	ATT	GTG	CTC	GTA	ACT	TGC	CTC	TTG	TTG	TTA	TGC	TCA	TAC	CAC	ACT	48
Met	Ile	Val	Leu	Val	Thr	Cys	Leu	Leu	Leu	Leu	Cys	Ser	Tyr	His	Thr	
1				5				10						15		
GTT	TCG	AGT	ACG	TCA	AAC	AAT	GAT	TGT	AGA	CAA	GTT	AAC	GTA	ACA	CAA	96
Val	Ser	Ser	Thr	Ser	Asn	Asn	Asp	Cys	Arg	Gln	Val	Asn	Val	Thr	Gln	
			20					25					30			
TTA	GCT	GGC	AAT	GAA	AAC	CTT	ATT	AGA	GAC	TTT	TTG	TTT	CAA	AGT	TTT	144
Leu	Ala	Gly	Asn	Glu	Asn	Leu	Ile	Arg	Asp	Phe	Leu	Phe	Gln	Ser	Phe	
		35					40					45				
AAA	GAA	GAA	GGA	ATT	GTA	GTT	GTT	GGT	GGT	TAT	TAC	CCT	ACA	GAG	GTG	192
Lys	Glu	Glu	Gly	Ile	Val	Val	Val	Gly	Gly	Tyr	Tyr	Pro	Thr	Glu	Val	
	50					55					60					
TGG	TAC	AAC	TGC	TCT	AGA	ACA	GCA	ACT	ACC	ACT	GCC	TAT	GAG	TAT	TTT	240
Trp	Tyr	Asn	Cys	Ser	Arg	Thr	Ala	Thr	Thr	Thr	Ala	Tyr	Glu	Tyr	Phe	
65					70				75						80	
AAT	AAT	ATA	CAT	GCC	TTT	TAT	TTT	GAT	ATG	GAA	GCT	ATG	GAA	AAT	AGC	288
Asn	Asn	Ile	His	Ala	Phe	Tyr	Phe	Asp	Met	Glu	Ala	Met	Glu	Asn	Ser	
				85					90					95		
ACT	GGT	AAT	GCA	CGT	GGT	AAA	CCT	CTA	TTA	TTT	CAT	GTT	CAT	GGT	GAA	336
Thr	Gly	Asn	Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	His	Gly	Glu	
			100					105					110			
CCT	GTT	AGT	ATC	ATC	ATA	TAT	ATA	TCA	GCT	TAT	GGG	GAT	GAT	GTG	CAA	384
Pro	Val	Ser	Ile	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Gly	Asp	Asp	Val	Gln	
		115					120					125				
CAA	AGG	CCA	CTT	TTA	GAA	CAT	GGG	TTA	TTG	TGC	ATT	ACT	AAA	AAT	CGC	432
Gln	Arg	Pro	Leu	Leu	Glu	His	Gly	Leu	Leu	Cys	Ile	Thr	Lys	Asn	Arg	
	130					135					140					
AAT	ATT	GAC	TAT	AAC	ACC	TTC	ACC	AGC	AAC	CAG	TGG	GAT	TCC	ATA	TGT	480
Asn	Ile	Asp	Tyr	Asn	Thr	Phe	Thr	Ser	Asn	Gln	Trp	Asp	Ser	Ile	Cys	
145					150					155					160	
ACG	GGT	AAT	GAC	AGA	AAA	ATT	CCT	TTC	TCT	GTC	ATA	CCC	AGG	GAT	AAT	528
Thr	Gly	Asn	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Arg	Asp	Asn	
				165				170						175		
GGA	ACA	AAA	ATC	TAT	GGG	CTT	GAG	TGG	AAT	GAT	GAA	TTT	GTT	ACA	GCG	576
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Glu	Phe	Val	Thr	Ala	
			180					185					190			
TAT	ATT	AGT	GGT	CGT	TCT	TAT	AAT	TGG	AAC	ATC	AAT	AAT	AAC	TGG	TTT	624
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	Asn	Trp	Asn	Ile	Asn	Asn	Asn	Trp	Phe	
		195					200					205				
AAC	AAT	GTC	ACA	CTT	TTG	TAT	TCA	CGC	TCA	AGC	ACT	GCT	ACC	TGG	GAA	672
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	
	210					215					220					
TAC	AGT	GCT	GCA	TAT	GTT	TAC	CAA	GGT	GTT	TCT	AAC	TTC	ACT	TAT	TAC	720
Tyr	Ser	Ala	Ala	Tyr	Val	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr	
225					230					235					240	
AAG	TTA	AAT	AAC	ACC	AAT	GGT	TTA	AAA	ACC	TAT	GAA	TTT	TGT	GAG	GAT	768
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Phe	Cys	Glu	Asp	
				245				250						255		



TAT GAA TAT TGC ACT GGC TAC GCC ACT AAT GTC TTT GCT CCA ACT GTG Tyr Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val 260 265 270	816
GGA GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTT TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGC TCC ACT TTT GTT AGT GGC AGA TTT GTA ACA AAC CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
CTA TTA GTT AAC TGC TTA TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCG CAG TTT AGT CAG TGT AGT GGT GTA Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Ser Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTA GAT GTT ATT AGA TTC AAT CTT AAT TTC ACC Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTG TTT TCG TTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACG GGT GGT GTC ATT CTT GAA GTT TCA TGT TAT AAT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Val Ser Cys Tyr Asn Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TTT TAC AGT TAT GGT GAA ATT CCG TTC GGC ATA ACT GAT Glu Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGG TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAG TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCT AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAC TTA ACC ACT GGT GAT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAC ACT GAG GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAG GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAG TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAG GTT GGT CTT GTG AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

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ATC	TTT	TTC	GCA	CAT	ACC	GCT	ATC	AAT	ATA	ACC	ATT	GAT	CTT	GGT	ATG	1632
Ile	Phe	Phe	Ala	His	Thr	Ala	Ile	Asn	Ile	Thr	Ile	Asp	Leu	Gly	Met	
530						535					540					
AAG	CGT	AGC	GGT	TAT	GGT	CAA	CCC	ATA	GCA	TCA	ACA	TTA	AGT	AAC	ATT	1680
Lys	Arg	Ser	Gly	Tyr	Gly	Gln	Pro	Ile	Ala	Ser	Thr	Leu	Ser	Asn	Ile	
545					550					555					560	
ACA	CTA	CCA	ATG	CAG	GAT	AAT	AAC	ACA	GAT	GTG	TAC	TGT	ATT	CGT	TCT	1728
Thr	Leu	Pro	Met	Gln	Asp	Asn	Asn	Thr	Asp	Val	Tyr	Cys	Ile	Arg	Ser	
				565					570					575		
AAC	CAG	TTT	TCA	GTT	TAT	GTT	CAT	TCT	ATT	TGT	AAG	AGT	TCT	TTA	TGG	1776
Asn	Gln	Phe	Ser	Val	Tyr	Val	His	Ser	Ile	Cys	Lys	Ser	Ser	Leu	Trp	
			580					585					590			
GAC	AAT	ATT	TTT	AAT	CAA	GAA	TGC	ACG	GAT	GTT	TTA	GAT	GCC	ACA	GCT	1824
Asp	Asn	Ile	Phe	Asn	Gln	Glu	Cys	Thr	Asp	Val	Leu	Asp	Ala	Thr	Ala	
		595					600					605				
GTT	ATA	AAG	ACT	GGT	ACT	TGT	CCT	TTC	TCA	TTT	GAT	AAA	TTG	AAC	AAT	1872
Val	Ile	Lys	Thr	Gly	Thr	Cys	Pro	Phe	Ser	Phe	Asp	Lys	Leu	Asn	Asn	
	610					615					620					
TAC	TTA	ACT	TTT	AAC	AAG	TTC	TGT	TTG	TCG	TTG	AGT	CCT	GTT	GGC	GCT	1920
Tyr	Leu	Thr	Phe	Asn	Lys	Phe	Cys	Leu	Ser	Leu	Ser	Pro	Val	Gly	Ala	
625					630					635					640	
AAC	TGC	AAG	TTT	GAT	GTT	GCC	GCA	CGT	ACA	AGA	ACC	AAT	GAG	CAA	GTT	1968
Asn	Cys	Lys	Phe	Asp	Val	Ala	Ala	Arg	Thr	Arg	Thr	Asn	Glu	Gln	Val	
				645				650						655		
GTT	AGA	AGT	CTA	TAT	GTA	ATA	TAT	GAA	GAA	GGA	GAC	AAC	ATA	GTT	GGT	2016
Val	Arg	Ser	Leu	Tyr	Val	Ile	Tyr	Glu	Glu	Gly	Asp	Asn	Ile	Val	Gly	
			660					665					670			
GTA	CCG	TCT	GAT	AAT	AGC	GGT	CTG	CAC	GAT	TTG	TCT	GTG	CTA	CAC	CTA	2064
Val	Pro	Ser	Asp	Asn	Ser	Gly	Leu	His	Asp	Leu	Ser	Val	Leu	His	Leu	
		675					680					685				
GAC	TCC	TGT	ACA	GAG	TAT	AAT	ATA	TAT	GGT	AGA	ACT	GGT	GTT	GGT	ATT	2112
Asp	Ser	Cys	Thr	Glu	Tyr	Asn	Ile	Tyr	Gly	Arg	Thr	Gly	Val	Gly	Ile	
	690					695					700					
ATT	AGA	CAA	ACT	AAC	AGT	ACG	CTA	CTT	AGC	GGC	TTA	TAT	TAC	ACA	TCA	2160
Ile	Arg	Gln	Thr	Asn	Ser	Thr	Leu	Leu	Ser	Gly	Leu	Tyr	Tyr	Thr	Ser	
705					710					715					720	
CTA	TCA	GGT	GAT	TTG	TTA	GGC	TTT	AAA	AAT	GTT	AGT	GAT	GGT	GTC	ATC	2208
Leu	Ser	Gly	Asp	Leu	Leu	Gly	Phe	Lys	Asn	Val	Ser	Asp	Gly	Val	Ile	
				725					730					735		
TAT	TCT	GTG	ACG	CCA	TGT	GAT	GTA	AGC	GCA	CAA	GCG	GCT	GTT	ATT	GAT	2256
Tyr	Ser	Val	Thr	Pro	Cys	Asp	Val	Ser	Ala	Gln	Ala	Ala	Val	Ile	Asp	
			740					745					750			
GGT	GCC	ATA	GTT	GGA	GCT	ATG	ACT	TCC	ATT	AAC	AGT	GAA	CTG	TTA	GGT	2304
Gly	Ala	Ile	Val	Gly	Ala	Met	Thr	Ser	Ile	Asn	Ser	Glu	Leu	Leu	Gly	
		755					760					765				
CTA	AAA	CAC	TGG	ACA	ACA	ACA	CCT	AAT	TTT	TAT	TAC	TAC	TCT	ATA	TAT	2352
Leu	Lys	His	Trp	Thr	Thr	Thr	Pro	Asn	Phe	Tyr	Tyr	Tyr	Ser	Ile	Tyr	
	770					775					780					
AAT	TAT	ACA	AAT	GAG	AGG	ACT	CGT	GGC	ACT	GCA	ATT	GAC	AGT	AAC	GAT	2400
Asn	Tyr	Thr	Asn	Glu	Arg	Thr	Arg	Gly	Thr	Ala	Ile	Asp	Ser	Asn	Asp	
785					790					795					800	

GTT GAT TGT GAA CCT ATC ATA ACC TAT TCT AAC ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815	2448
AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAT GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830	2496
CAA CCA ATT AGC ACT GGT ACT GTC ACG ATA CCT ACA AAC TTT ACC ATA Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845	2544
TCT GTG CAA GTC GAA TAC ATT CAG GTT TAC ACC ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile 850 855 860	2592
GAT TGT GCA AGA TAC GTT TGC AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880	2640
TTA ACA CAA TAT GTT TCT GCA TGT CAA ACT ATT GAG CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895	2688
ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTC GTT Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910	2736
TCT GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925	2784
GAA AAT TTA GAC CCT ATT TAC AAA GAA TGG CCT AAC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser 930 935 940	2832
TGG TTA GGA GGT TTA AAA GAC ATA CTG CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960	2880
AAG TAT CGT TCT GCT ATA GAA GAC TTG CTT TTT GAT AAG GTT GTA ACT Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975	2928
TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACA GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990	2976
TAT GAC ATA GCC GAC TTA GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005	3024
GTG TTA CCT GGT GTA GCT AAT GAT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020	3072
TCT CTT GCA GGT GGT ATA ACA CTA GGT GCA CTT GGT GGT GGC GCC GTT Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val 1025 1030 1035 1040	3120
GCT ATA CCT TTT GCA GTA GCA GTT CAA GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055	3168
CTA CAA ACT GAT GTA TTG AAT AAA AAC CAG CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070	3216

TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCA TTT GGC AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA AAA GGT CTT GCA ACT GTT GCT AAA GCA Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGC Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTA ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGC TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGA AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCG GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAG GAC AAG GTT AAT GAA TGT GTT AGA TCC CAA TCT CAG AGA TTT Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAC TTG TTT TCA CTT GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTG CTA TTA CCA ACG GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG CCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744
ACT TTT GGA CTT GTC GTT AAA GAT GTA CAG TTG ACG TTG TTT CGT AAC Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACT CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GCT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAG GGG TGC GAT GTG TTG Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAT GCA ACT GTA ATT GAC TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATC AAT CAG ACT GTT CAA GAT ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTG ACA CTT GAT ATT TTT AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340	4032

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TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAA TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAC AAT ACC ACT GTA GAA CTT GCC ATT CTC ATT GAC AAC ATT AAC Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn 1365 1370 1375	4128
AAC ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTA ATA GGC TTA GTA GTA ATA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe 1395 1400 1405	4224
TGC ATA CCA TTA TTG CTA TTT TGC TGT TGT AGT ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGC TTA GGA AGT TGT TGT CAC TCT ATG TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
TAA	4365

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15
Val Ser Ser Thr Ser Asn Asn Asp Cys Arg Gln Val Asn Val Thr Gln 20 25 30
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Gln Ser Phe 35 40 45
Lys Glu Glu Gly Ile Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60
Trp Tyr Asn Cys Ser Arg Thr Ala Thr Thr Thr Ala Tyr Glu Tyr Phe 65 70 75 80
Asn Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser 85 90 95
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110
Pro Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Gly Asp Asp Val Gln 115 120 125



Gln	Arg	Pro	Leu	Leu	Glu	His	Gly	Leu	Leu	Cys	Ile	Thr	Lys	Asn	Arg
130						135					140				
Asn	Ile	Asp	Tyr	Asn	Thr	Phe	Thr	Ser	Asn	Gln	Trp	Asp	Ser	Ile	Cys
145					150					155					160
Thr	Gly	Asn	Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Arg	Asp	Asn
				165					170					175	
Gly	Thr	Lys	Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Glu	Phe	Val	Thr	Ala
			180					185					190		
Tyr	Ile	Ser	Gly	Arg	Ser	Tyr	Asn	Trp	Asn	Ile	Asn	Asn	Asn	Trp	Phe
		195					200					205			
Asn	Asn	Val	Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu
	210					215					220				
Tyr	Ser	Ala	Ala	Tyr	Val	Tyr	Gln	Gly	Val	Ser	Asn	Phe	Thr	Tyr	Tyr
225					230					235					240
Lys	Leu	Asn	Asn	Thr	Asn	Gly	Leu	Lys	Thr	Tyr	Glu	Phe	Cys	Glu	Asp
				245					250					255	
Tyr	Glu	Tyr	Cys	Thr	Gly	Tyr	Ala	Thr	Asn	Val	Phe	Ala	Pro	Thr	Val
			260					265					270		
Gly	Gly	Tyr	Ile	Pro	Asp	Gly	Phe	Ser	Phe	Asn	Asn	Trp	Phe	Leu	Leu
		275					280					285			
Thr	Asn	Ser	Ser	Thr	Phe	Val	Ser	Gly	Arg	Phe	Val	Thr	Asn	Gln	Pro
	290					295					300				
Leu	Leu	Val	Asn	Cys	Leu	Trp	Pro	Val	Pro	Ser	Phe	Gly	Val	Ala	Ala
305					310					315					320
Gln	Glu	Phe	Cys	Phe	Glu	Gly	Ala	Gln	Phe	Ser	Gln	Cys	Ser	Gly	Val
				325					330					335	
Ser	Leu	Asn	Asn	Thr	Val	Asp	Val	Ile	Arg	Phe	Asn	Leu	Asn	Phe	Thr
			340					345					350		
Ala	Asp	Val	Gln	Ser	Gly	Met	Gly	Ala	Thr	Val	Phe	Ser	Leu	Asn	Thr
		355					360					365			
Thr	Gly	Gly	Val	Ile	Leu	Glu	Val	Ser	Cys	Tyr	Asn	Asp	Thr	Val	Ser
	370					375					380				
Glu	Ser	Ser	Phe	Tyr	Ser	Tyr	Gly	Glu	Ile	Pro	Phe	Gly	Ile	Thr	Asp
385					390					395					400
Gly	Pro	Arg	Tyr	Cys	Tyr	Val	Leu	Tyr	Asn	Gly	Thr	Ala	Leu	Lys	Tyr
				405					410					415	
Leu	Gly	Thr	Leu	Pro	Pro	Ser	Val	Lys	Glu	Ile	Ala	Ile	Ser	Lys	Trp
			420					425					430		
Gly	His	Phe	Tyr	Ile	Asn	Gly	Tyr	Asn	Phe	Phe	Ser	Thr	Phe	Pro	Ile
		435					440					445			
Asp	Cys	Ile	Ser	Phe	Asn	Leu	Thr	Thr	Gly	Asp	Ser	Gly	Ala	Phe	Trp
	450					455					460				
Thr	Ile	Ala	Tyr	Thr	Ser	Tyr	Thr	Glu	Ala	Leu	Val	Gln	Val	Glu	Asn
465					470					475					480



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Thr	Ala	Ile	Lys	Lys	Val	Thr	Tyr	Cys	Asn	Ser	His	Ile	Asn	Asn	Ile
				485					490					495	
Lys	Cys	Ser	Gln	Leu	Thr	Ala	Asn	Leu	Asn	Asn	Gly	Phe	Tyr	Pro	Val
			500					505					510		
Ala	Ser	Ser	Glu	Val	Gly	Leu	Val	Asn	Lys	Ser	Val	Val	Leu	Leu	Pro
			515				520					525			
Ile	Phe	Phe	Ala	His	Thr	Ala	Ile	Asn	Ile	Thr	Ile	Asp	Leu	Gly	Met
	530					535					540				
Lys	Arg	Ser	Gly	Tyr	Gly	Gln	Pro	Ile	Ala	Ser	Thr	Leu	Ser	Asn	Ile
545					550					555					560
Thr	Leu	Pro	Met	Gln	Asp	Asn	Asn	Thr	Asp	Val	Tyr	Cys	Ile	Arg	Ser
				565					570					575	
Asn	Gln	Phe	Ser	Val	Tyr	Val	His	Ser	Ile	Cys	Lys	Ser	Ser	Leu	Trp
			580					585					590		
Asp	Asn	Ile	Phe	Asn	Gln	Glu	Cys	Thr	Asp	Val	Leu	Asp	Ala	Thr	Ala
		595					600					605			
Val	Ile	Lys	Thr	Gly	Thr	Cys	Pro	Phe	Ser	Phe	Asp	Lys	Leu	Asn	Asn
	610					615					620				
Tyr	Leu	Thr	Phe	Asn	Lys	Phe	Cys	Leu	Ser	Leu	Ser	Pro	Val	Gly	Ala
625					630					635					640
Asn	Cys	Lys	Phe	Asp	Val	Ala	Ala	Arg	Thr	Arg	Thr	Asn	Glu	Gln	Val
				645					650					655	
Val	Arg	Ser	Leu	Tyr	Val	Ile	Tyr	Glu	Glu	Gly	Asp	Asn	Ile	Val	Gly
			660					665					670		
Val	Pro	Ser	Asp	Asn	Ser	Gly	Leu	His	Asp	Leu	Ser	Val	Leu	His	Leu
			675				680					685			
Asp	Ser	Cys	Thr	Glu	Tyr	Asn	Ile	Tyr	Gly	Arg	Thr	Gly	Val	Gly	Ile
						695					700				
Ile	Arg	Gln	Thr	Asn	Ser	Thr	Leu	Leu	Ser	Gly	Leu	Tyr	Tyr	Thr	Ser
705					710					715					720
Leu	Ser	Gly	Asp	Leu	Leu	Gly	Phe	Lys	Asn	Val	Ser	Asp	Gly	Val	Ile
				725					730					735	
Tyr	Ser	Val	Thr	Pro	Cys	Asp	Val	Ser	Ala	Gln	Ala	Ala	Val	Ile	Asp
			740					745					750		
Gly	Ala	Ile	Val	Gly	Ala	Met	Thr	Ser	Ile	Asn	Ser	Glu	Leu	Leu	Gly
		755					760					765			
Leu	Lys	His	Trp	Thr	Thr	Thr	Pro	Asn	Phe	Tyr	Tyr	Tyr	Ser	Ile	Tyr
	770					775					780				
Asn	Tyr	Thr	Asn	Glu	Arg	Thr	Arg	Gly	Thr	Ala	Ile	Asp	Ser	Asn	Asp
785					790					795					800
Val	Asp	Cys	Glu	Pro	Ile	Ile	Thr	Tyr	Ser	Asn	Ile	Gly	Val	Cys	Lys
				805					810					815	
Asn	Gly	Ala	Leu	Val	Phe	Ile	Asn	Val	Thr	His	Ser	Asp	Gly	Asp	Val
			820					825					830		

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Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile  
 835 840 845  
 Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile  
 850 855 860  
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu  
 865 870 875 880  
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala  
 885 890 895  
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val  
 900 905 910  
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr  
 915 920 925  
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser  
 930 935 940  
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg  
 945 950 955 960  
 Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr  
 965 970 975  
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly  
 980 985 990  
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met  
 995 1000 1005  
 Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala  
 1010 1015 1020  
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val  
 1025 1030 1035 1040  
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala  
 1045 1050 1055  
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070  
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085  
 Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100  
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120  
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135  
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150  
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165  
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180  
 Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe

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1185	1190	1195	1200
Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala	1205	1210	1215
Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr	1220	1225	1230
Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg	1235	1240	1245
Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn	1250	1255	1260
Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg	1265	1270	1275
Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu	1285	1290	1295
Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr	1300	1305	1310
Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro	1315	1320	1325
Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr	1330	1335	1340
Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys	1345	1350	1355
Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn	1365	1370	1375
Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val	1380	1385	1390
Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe	1395	1400	1405
Cys Ile Pro Leu Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly	1410	1415	1420
Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg	1425	1430	1435
Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His	1445	1450	

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2244

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGATTGTGC TCGTAACTTG CCTCTTGTTG TTATGTTTCAT ACCACACAGT TTTGAGTACA	60
ACAAATAATG AATGCATACA AGTTAACGTA ACACAATTGG CTGGCAATGA AAACCTTATC	120
AGAGATTTTC TGTTTAGTAA CTTTAAAGAA GAAGGAAGTG TAGTTGTTGG TGGTTATTAC	180
CCTACAGAGG TGTGGTACAA CTGCTCTAGA ACAGCTCGAA CTACTGCCTT TCAGTATTTT	240
AATAATATAC ATGCCTTTTA TTTTGTTATG GAAGCCATGG AAAATAGCAC TGGTAATGCA	300
CGTGGTAAAC CATTATTATT TCATGTGCAT GGTGAGCCTG TTAGTGTTAT TATATATATA	360
TCGGCTTATA GGGATGATGT GCAACAAAGG CCCCTTTTAA AACATGGGTT AGTGTGCATA	420
ACTAAAATC GCCATATTAA CTATGAACAA TTCACCTCCA ACCAGTGGA TCCACATGT	480
ACGGGTGCTG ACAGAAAAAT TCCTTTCTCT GTCATACCCA CGGACAATGG AACAAAAATC	540
TATGGTCTTG AGTGGAATGA TGACTTTGTT ACAGCTTATA TTAGTGGTCG TTCTTATCAC	600
TTGAACATCA ATACTAATTG GTTTAACAAT GTCACACTTT TGTATTCACG CTCAAGCACT	660
GCTACCTGGG AATACAGTGC TGCATATGCT TACCAAGGTG TTTCTAACTT CACTTATTAC	720
AAGTTAAATA ACACCAATGG TCTAAAAACC TATGAATTAT GTGAAGATTA TGAACATTGC	780
ACTGGCTATG CTACCAATGT ATTTGCTCCG ACATCAGGTG GTTACATACC TGATGGATTT	840
AGTTTTAAYA ATTGGTTCTT GCTTACAAAT AGTTCCACTT TTGTTAGTGG CAGGTTTGTA	900
ACAAATCAAC CATTATTGAT TAATTGCTTG TGGCCAGTGC CCAGTTTTGG TGTAGCAGCA	960
CAAGAATTTT GTTTGAAGG TGCACAGTTT AGCCAATGTA ATGGTGTGTC TTTAAATAAC	1020
ACAGTGGATG TTATTAGATT CAACCTTAAT TTCACTGCAG ATGTACAATC TGGTATGGGT	1080
GCTACAGTAT TTCACTGAA TACAACAGGT GGTGTCATTC TTGAAATTC ATGTTATAGT	1140
GACACAGTGA GTGAGTCTAG TTCTTACAGT TATGGTGAAA TCCCGTTCGG CATAACTGAC	1200
GGACCACGAT ACTGTTATGT ACTTTACAAT GGCACAGCTC TTAAATATTT AGGAACATTA	1260
CCACCCAGTG TAAAGGAAAT TGCTATTAGT AAGTGGGGCC ATTTTATAT TAATGGTTAC	1320
AATTTCTTTA GCACATTTCC TATTGRTTGT ATATCTTTTA ATTTAACCAC TGGTGTTAGT	1380
GGAGCTTTTT GGACAATTGC TTACACATCG TATACTGAAG CATTAGTACA AGTTGAAAAC	1440
ACAGCTATTA AAAATGTGAC GTATTGTAAC AGTCACATTA ATAACATTAA ATGTTCTCAA	1500
CTTACTGCTA ATTTGAATAA TGGATTTTAT CCTGTTGCTT CAAGTGAAGT AGGTTTCGTT	1560
AATAAGAGTG TTGTGTTATT ACCTAGCTTT TTCACATACA CCGCTGTCAA TATAACCATT	1620
GATCTTGGTA TGAAGCTTAG TGGTTATGGT CAACCCATAG CCTCGACACT AAGTAACATC	1680
ACACTACCAA TGCAGGATAA CAATACTGAT GTGTACTGTA TTCGTTCTAA CCAATTCTCA	1740
GTTTATGTTT ATTCCACTTG CAAAAGTTCT TTATGGGACA ATATTTTAA TCAAGACTGC	1800
ACGGATGTTT TAGAGGCTAC AGCTGTTATA AAAACTGGTA CTTGTCCTTT CTCATTGAT	1860
AAATTGAACA ATTACTTGAC TTTTAACAAG TTCTGTTTGT CGTTGAGTCC TGTTGGTGCT	1920
AATTGCAAGT TTGATGTTGC TGCACGTACA AGAACCAATG AGCAGGTTGT TAGAAGTCTA	1980

TATGTAATAT ATGAAGAAGG AGACAACATA GTGGGTGTAC CGTCTGATRA TAGCGGTCTG 2040  
 CACGATTTGT CTGTGCTACA CCTAGACTCC TGTACAGATT ACAATATATA TGGTAGAACT 2100  
 GGTGTTGGTA TTATTAGACG AACTAACAGT ACGCTACTTA GTGGCTTATA TTACACATCA 2160  
 CTATCAGGTG ATTTGTTAGG CTTTAAAAAT GTTAGTGATG GTGTCATTTA TTCTGTGACG 2220  
 CCATGTGATG TAAGCGCACA AGCGGC 2246

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr  
 1 5 10 15  
 Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln  
 20 25 30  
 Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe  
 35 40 45  
 Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val  
 50 55 60  
 Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe  
 65 70 75 80  
 Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser  
 85 90 95  
 Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu  
 100 105 110  
 Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln  
 115 120 125  
 Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg  
 130 135 140  
 His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys  
 145 150 155 160  
 Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn  
 165 170 175  
 Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala  
 180 185 190  
 Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe  
 195 200 205  
 Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu  
 210 215 220  
 Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
 225 230 235 240

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Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
 245 250 255  
 Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
 260 265 270  
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
 275 280 285  
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
 290 295 300  
 Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
 305 310 315 320  
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
 325 330 335  
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
 340 345 350  
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
 355 360 365  
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
 370 375 380  
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
 385 390 395 400  
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
 405 410 415  
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
 420 425 430  
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
 435 440 445  
 Xaa Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
 450 455 460  
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
 465 470 475 480  
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
 485 490 495  
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
 500 505 510  
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
 515 520 525  
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
 530 535 540  
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
 545 550 555 560  
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
 565 570 575  
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590



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Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Xaa Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700  
 Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720  
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735  
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCG AGT ACG TCA AAC AAT GAT TGT AGA  
 Ser Ser Thr Ser Asn Asn Asp Cys Arg  
 1 5

27

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Thr Ser Asn Asn Asp Cys Arg  
 1 5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Ser Phe Lys Glu Glu Gly Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

18

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ala Thr Thr Thr Ala Tyr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..150

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGG GAT GAT GTG CAA CAA AGG CCA CTT TTA GAA CAT GGG TTA TTG TGC	48
Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys	
1 5 10 15	
ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC AAC CAG	96
Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln	
20 25 30	
TGG GAT TCC ATA TGT ACG GGT AAT GAC AGA AAA ATT CCT TTC TCT GTC	144
Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val	
35 40 45	
ATA CCC	150
Ile Pro	
50	

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys	
1 5 10 15	
Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln	
20 25 30	
Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val	
35 40 45	
Ile Pro	
50	

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAT ATT GAC TAT AAC ACC  
 Asn Ile Asp Tyr Asn Thr  
 1 5

18

## (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asn Ile Asp Tyr Asn Thr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTG TGC ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC  
 Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser  
 1 5 10 15

48

AAC CAG TGG GAT TCC ATA  
 Asn Gln Trp Asp Ser Ile  
 20

66

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

137

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser  
 1 5 10 15  
 Asn Gln Trp Asp Ser Ile  
 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAT CGC AAT ATT GAC TAT AAC ACC  
 Asn Arg Asn Ile Asp Tyr Asn Thr  
 1 5

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Arg Asn Ile Asp Tyr Asn Thr  
 1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAT TGG AAC ATC AAT AAT  
 Asn Trp Asn Ile Asn Asn  
 1 5

18

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asn Trp Asn Ile Asn Asn  
1 5

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATC TTT TTC GCA CAT ACC GCT ATC  
Ile Phe Phe Ala His Thr Ala Ile  
1 5

24

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Phe Phe Ala His Thr Ala Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..375



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AAT GCT CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT	48
Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val	
1 5 10 15	
AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG	96
Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg	
20 25 30	
CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT	144
Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile	
35 40 45	
AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT	192
Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly	
50 55 60	
GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA	240
Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr	
65 70 75 80	
AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT	288
Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile	
85 90 95	
AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT	336
Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn	
100 105 110	
GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GA	377
Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp	
115 120 125	

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val	
1 5 10 15	
Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg	
20 25 30	
Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile	
35 40 45	
Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly	
50 55 60	
Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr	
65 70 75 80	
Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile	
85 90 95	

Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn  
100 105 110  
Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp  
115 120 125